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(m64347)  
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(7129)

**Full Record****Details for HUGENEFL:M64347\_AT****Full Screen**

**NetAffx Links** [Cluster Members](#)  
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**GeneChip Array Information**

**Probe Set ID** M64347\_at  
**GeneChip  
Array** HumanGeneFL Array  
**Organism  
Common  
Name** Human

**Probe Design Information**

**Transcript ID** M64347  
**Sequence  
Type** Exemplar sequence  
**Representative  
Public ID** M64347 [NCBI](#)  
**Target  
Description** M64347, class A, 20 probes, 20 in M64347 3336-3720, Human novel growth factor receptor mRNA, 3' cds

**Genomic Alignment of Target Sequence**

**Assembly** April 2003 (NCBI 33)  
**Alignment(s)**

	Position	% Identity	Cytoband
chr4: 1771773-1772182 (+)	<a href="#">UCSC</a>	93	p16.3

	Representative Transcript	UniGene Description	Position
<b>Overlapping Transcripts</b>	NM_000142 <a href="#">NCBI</a>	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	chr4:1757261- 1772237 (+) <a href="#">UCSC</a>
	NM_022965 <a href="#">NCBI</a>	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	chr4:1757261- 1772237 (+) <a href="#">UCSC</a>

**Public Domain and Genome References**

**Gene Title** fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)  
**Gene Symbol** FGFR3 [HGNC](#)  
**Chromosomal  
Location** 4p16.3  
**UniGene ID** Hs.1420 [NCBI](#) (FULL LENGTH)  
**Ensembl** ENSG00000068078 [Ensembl](#)  
**LocusLink** 2261 [NCBI](#)  
P22607 [EMBL-EBI](#)

SwissProt	Q96T34	<a href="#">EMBL-EBI</a>
	Q96T35	<a href="#">EMBL-EBI</a>
	Q96T36	<a href="#">EMBL-EBI</a>
	Q9NRB6	<a href="#">EMBL-EBI</a>
EC	2.7.1.112	
OMIM	134934	<a href="#">NCBI</a>
RefSeq Protein ID	NP_000133	<a href="#">NCBI</a>
	NP_075254	<a href="#">NCBI</a>
RefSeq	RefSeq Transcript ID      RefSeq Title	
	NM_000142	<a href="#">NCBI</a> fibroblast growth factor receptor 3 isoform 1 precursor
	NM_022965	<a href="#">NCBI</a> fibroblast growth factor receptor 3 isoform 2 precursor

## Functional Annotations

	ID	Title	Organism	Type
Ortholog	<a href="#">DROSGENOME1:143549_AT</a>	breathless	Drosophila	Putative Ortholog
	<a href="#">RAE230A:1369373_AT</a>	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	<a href="#">RAE230B:1384056_AT</a>	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	<a href="#">RAE230B:1384829_AT</a>	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	<a href="#">RG-U34B:RC_AA899336_AT</a>	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	<a href="#">RG-U34C:RC_AI136304_AT</a>	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	<a href="#">RG-U34C:RC_AI145424_AT</a>	fibroblast growth factor receptor 3	Rat	Putative Ortholog
	<a href="#">MG-U74AV2:160919_R_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MG-U74AV2:162253_I_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MOE430A:1421841_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MOE430A:1425796_A_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MU11KSUBA:M81342_S_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MOUSE430_2:1421841_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MOUSE430_2:1425796_A_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MOUSE430A_2:1421841_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog
	<a href="#">MOUSE430A_2:1425796_A_AT</a>	fibroblast growth factor receptor 3	Mouse	Curated Ortholog

## GO Biological Process (view graph)

ID	Description	Evidence	Links
165	MAPKKK cascade	experimental evidence	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
1501	skeletal development	predicted/computed	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
7048	oncogenesis	experimental evidence	<a href="#">QuickGO</a> <a href="#">AmiGO</a>
7259	JAK-STAT cascade	experimental	<a href="#">QuickGO</a>

8543 FGF receptor signaling pathway		evidence experimental evidence	<a href="#">AmiGO</a> <a href="#">QuickGO</a> <a href="#">AmiGO</a>
GO Cellular Component (view graph)			
Gene Ontology	ID	Description	Evidence
	5887	integral to plasma membrane	experimental evidence <a href="#">QuickGO</a> <a href="#">AmiGO</a>
GO Molecular Function (view graph)			
	ID	Description	Evidence
	5007	fibroblast growth factor receptor activity	experimental evidence <a href="#">QuickGO</a> <a href="#">AmiGO</a>
Protein Similarities	Method	ID	Description
	blast	13112048	fibroblast growth factor receptor 3 isoform 2 precursor; hydroxyaryl-protein kinase; tyrosine kinase JTK4 [Homo sapiens]
	blast	13186255	fibroblast growth factor receptor 2 isoform 3 precursor; keratinocyte growth factor receptor; K-sam protein; protein tyrosine kinase, receptor like 14; FGF receptor; bacteria-expressed kinase; fibroblast growth factor receptor BEK; tyrosylprotein kinase; hydroxyaryl-protein kinase [Homo sapiens]
	blast	4503711	fibroblast growth factor receptor 3 isoform 1 precursor; hydroxyaryl-protein kinase; tyrosine kinase JTK4 [Homo sapiens]
	blast	20452380	
Protein Families	Method	ID	Description
	Hanks	<a href="#">FGFR-3</a>	FGR3_HUMAN (FGFR-3) KINASES:5.6.3   PTK Group B membrane spanning protein tyrosine kinases.PTK XV Fibroblast growth factor receptor family .FGFR-3
	ec	<a href="#">ZA70_HUMAN</a>	ZA70_HUMAN EC:2.7.1.112:TYROSINE-PROTEIN KINASE ZAP-70 (EC 2.7.1.112) (70 KDA ZETA-ASSOCIATED PROTEIN) (SYK-RELATED TYROSINE KINASE).
	Hanks	<a href="#">FGFR-3</a>	FGR3_HUMAN (FGFR-3) KINASES:5.6.3   PTK Group B membrane spanning protein tyrosine kinases.PTK XV Fibroblast growth factor receptor family .FGFR-3
	ec	<a href="#">ZA70_HUMAN</a>	ZA70_HUMAN EC:2.7.1.112:TYROSINE-PROTEIN KINASE ZAP-70 (EC 2.7.1.112) (70 KDA ZETA-ASSOCIATED PROTEIN) (SYK-RELATED TYROSINE KINASE).
	Database	ID	Description
	scop	<a href="#">d1gjoa_</a>	d1gjoa_ SCOP:d.144.1.2:  Fibroblast growth factor receptor 2
	scop	<a href="#">d1ev2e1</a>	d1ev2e1 SCOP:b.1.1.4:  Fibroblast growth factor receptor, FGFR
	scop	<a href="#">d1gjoa_</a>	d1gjoa_ SCOP:d.144.1.2:  Fibroblast growth factor receptor 2

Protein Domains	scop	<u>d1ev2e1</u>	d1ev2e1 SCOP:b.1.1.4:  Fibroblast growth factor receptor, FGFR	4.25E-21
	pfam	<u>ig</u>	Immunoglobulin domain	1.6E-5
	pfam	<u>ig</u>	Immunoglobulin domain	3.2E-8
	pfam	<u>pkinase</u>	Protein kinase domain	2.3E-92
	pfam	<u>ig</u>	Immunoglobulin domain	1.6E-5
	pfam	<u>ig</u>	Immunoglobulin domain	3.2E-8
	pfam	<u>pkinase</u>	Protein kinase domain	2.3E-92
	pfam	<u>ig</u>	Immunoglobulin domain	7.3E-8
	InterPro	IPR000719 <u>EMBL-EBI</u>	Protein kinase	
	InterPro	IPR007110 <u>EMBL-EBI</u>	Immunoglobulin-like	
Protein Domains	InterPro	IPR001245 <u>EMBL-EBI</u>	Tyrosine protein kinase	
	InterPro	IPR008266 <u>EMBL-EBI</u>	Tyrosine protein kinase, active site	
	InterPro	IPR003598 <u>EMBL-EBI</u>	Immunoglobulin C-2 type	

## Trans Membrane

ID	Number Of Domains	Probability of Interior N-Terminus
NP_000133	2	0.11005

## Sequence

>HUGENEFL:M64347\_AT  
gacttcaaagcaagctggtatTTTTcatacaaattcttctaattgctgtgtgtcccaggca  
gggagacggtttccaggaggggcccctgtgtgcagggtccgatgttattagatgtt  
acaagtttatatatatatatatataatttattgagttttacaagatgtatttgtgt  
agacttaacacttcttacgcaatgcttctagagttttatagcctggactgctaccttca  
aagcttggaggggaagccgtgaattcagttggttcgttctgtactgttactgggcccctgag  
tctgggcagctgtcccttgcttgccctgcagggccatggctcaggggtggtctcttcttggg  
gcccagtgcatggtggccagaggtgtcacccaaaccggcaggtgcgatt

## Target Sequence

Probe Info	Probe Sequence(5'-3')	Probe		Probe Interrogation Position	Strandedness
		X	Y		
	GACTTCAAAGCAAGCTGGTATTTTC	359	161	3348	Antisense
	CATACAAATTCTTCTAATTGCTGTG	360	161	3372	Antisense
	AATTCTTCTAATTGCTGTGTGTCCC	361	161	3378	Antisense
	TGCTGTGTGTCCCAGGCAGGGAGAC	362	161	3390	Antisense
	TGTGTGCAGGTTCCGATGTTATTAG	363	161	3438	Antisense
	TCTTACGCAATGCTTCTAGAGTTTT	364	161	3540	Antisense
	GCAATGCTTCTAGAGTTTTATAGCC	365	161	3546	Antisense
	GAGTTTTATAGCCTGGACTGCTACC	366	161	3558	Antisense
	TGCTACCTTTCAAAGCTTGGAGGGA	367	161	3576	Antisense
	AAGCTTGGAGGGAAGCCGTGAATTC	368	161	3588	Antisense
	TGAATTCAGTTGGTTCGTTCTGTAC	369	161	3606	Antisense
	GTTTCGTTCTGTACTGTTACTGGGCC	370	161	3618	Antisense
	CTGGGCCCTGAGTCTGGGCAGCTGT	371	161	3636	Antisense
	CCTGAGTCTGGGCAGCTGTCCCTTG	372	161	3642	Antisense
	TCTGGGCAGCTGTCCCTTGCTTGCC	373	161	3648	Antisense
	TCCCTTGCTTGCCCTGCAGGGCCATG	374	161	3660	Antisense

GCTTGCCTGCAGGGCCATGGCTCAG	375	161	3666	Antisense
CTTGGGGCCCAGTGCATGGTGGCCA	376	161	3702	Antisense
GTGGCCAGAGGTGTCACCCAAACCG	377	161	3720	Antisense
GTCACCCAAACCGGCAGGTGCGATT	378	161	3732	Antisense

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